

<!--StartFragment-->RESULT 1

AAW10593

ID AAW10593 standard; protein; 257 AA.

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AC AAW10593;

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DT 15-JUN-2007 (revised)

DT 29-OCT-1997 (first entry)

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DE Hevea brasiliensis S-hydroxynitrilase.

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KW S-hydroxynitrilase; chiral synthesis; aliphatic; aromatic; S-cyanohydrin;
KW recombinant; BOND_PC; hydroxynitrile lyase; G016829; G046991; G08152.

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OS Hevea brasiliensis.

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PN W09703204-A2.

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PD 30-JAN-1997.

XX

PF 10-JUL-1996; 96WO-EP003010.

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PR 12-JUL-1995; 95AT-00001182.

XX

PA (STAM) DSM CHEMIE LINZ GMBH.

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PI Hasslacher M, Schall M, Schwab H, Hayn EM, Kohlwein S, Griengl H;

XX

DR WPI; 1997-119058/11.

DR N-PSDB; AAT36351.

DR PC:NCBI; gi1708278.

DR PC:SWISSPROT; P52704.

DR PC:BIND; 229823,256092,229822,256091,74321.

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PT Hevea brasiliensis S-hydroxy:nitrilase - and recombinant equivalent of
PT high specific activity, for chiral synthesis of cyano:hydrin(s).

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PS Claim 2; Page 2-3; 14pp; German.

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CC The present sequence is the Hevea brasiliensis S-hydroxynitrilase (S-HN),
CC which can be used for the chiral synthesis of aliphatic or aromatic S-
CC cyanohydrins from HCN, or its donor, and ketone. Recombinant S-HN has
CC higher specific activity than the native enzyme. H. brasiliensis leaves
CC were homogenised in cold pH 6.5 K phosphate buffer, and the extract
CC subjected to sequential chromatography on QAE-Sepharose, Phenyl-Sepharose
CC and BioGel 150 to recover a protein with a specific activity of 19 IU/mg.
CC A cDNA library was prepared from young H. brasiliensis leaves in Zap
CC phage, and screened with polyclonal rabbit antiserum raised against the
CC purified enzyme. The insert in one positive clone was isolated, and

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.

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SQ Sequence 257 AA;

Query Match 100.0%; Score 1370; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.9e-138;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  MAFAHFVLIHTICHGAWIWHKLKPLLEALGHKVTALDLAASGVDPQRQIEEIGSFDEYSEP  60
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Db      1  MAFAHFVLIHTICHGAWIWHKLKPLLEALGHKVTALDLAASGVDPQRQIEEIGSFDEYSEP  60

Qy     61  LLTFLEALPPGEKVIILVGESCGGLNIAIAADKYCEKIAAAVFHNSVLPDTEHCPSYVVDK  120
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Db     61  LLTFLEALPPGEKVIILVGESCGGLNIAIAADKYCEKIAAAVFHNSVLPDTEHCPSYVVDK  120

Qy    121  LMEVFPDWKDDTTYFTYTKDGKEITGLKLGFTLLRENLYTLCGPPEEYELAKMLTRKGS LFQ  180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  LMEVFPDWKDDTTYFTYTKDGKEITGLKLGFTLLRENLYTLCGPPEEYELAKMLTRKGS LFQ  180

Qy    181  NILAKRPFFTKEGYGSIKKIYVWTDQDEIFLPEFQLWQIENYKPDVKYKVEGGDHLQLT  240
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Db    181  NILAKRPFFTKEGYGSIKKIYVWTDQDEIFLPEFQLWQIENYKPDVKYKVEGGDHLQLT  240

Qy    241  KTKEIAEILQEVA DTYN  257
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Db    241  KTKEIAEILQEVA DTYN  257
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